

OIIPE

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## RAW SEQUENCE LISTING

DATE: 08/14/2001

PATENT APPLICATION: US/09/785,215

TIME: 12:01:30

Input Set : A:\3631-0107P.ST25.txt

Output Set: N:\CRF3\08142001\I785215.raw

3 <110> APPLICANT: JENSEN, Martin Roland et al.  
 5 <120> TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID  
 7 <130> FILE REFERENCE: 3631-0107P  
 9 <140> CURRENT APPLICATION NUMBER: 09/785,215  
 10 <141> CURRENT FILING DATE: 2001-02-20  
 12 <160> NUMBER OF SEQ ID NOS: 19  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 2313  
 18 <212> TYPE: DNA  
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 33 <220> FEATURE:  
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 36 <223> OTHER INFORMATION: Nucleotides encoding C-100  
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 42 <223> OTHER INFORMATION: Abeta 42/43  
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 46 <221> NAME/KEY: misc\_feature  
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 48 <223> OTHER INFORMATION: Abeta 42/43

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 54 1 5 10 15  
 56 gcg ctg gag gta ccc act gat ggt aat gct ggc ctg ctg gct gaa ccc 96  
 57 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
 58 20 25 30  
 60 cag att gcc atg ttc tgt ggc aga ctg aac atg cac atg aat gtc cag 144  
 61 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 62 35 40 45  
 64 aat ggg aag tgg gat tca gat cca tca ggg acc aaa acc tgc att gat 192  
 65 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 66 50 55 60  
 68 acc aag gaa ggc atc ctg cag tat tgc caa gaa gtc tac cct gaa ctg 240  
 69 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
 70 65 70 75 80

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72	cag	atc	acc	aat	gtg	gta	gaa	gcc	aac	caa	cca	gtg	acc	atc	cag	aac	288
73	Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn	
74					85				90						95		
76	tgg	tgc	aag	cgg	ggc	cgc	aag	cag	tgc	aag	acc	cat	ccc	cac	ttt	gtg	336
77	Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val	
78				100				105						110			
80	att	ccc	tac	cgc	tgc	tta	gtt	ggt	gag	ttt	gta	agt	gat	gcc	ctt	ctc	384
81	Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu	
82			115					120					125				
84	gtt	cct	gac	aag	tgc	aaa	ttc	tta	cac	cag	gag	agg	atg	gat	gtt	tgc	432
85	Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys	
86		130					135					140					
88	gaa	act	cat	ctt	cac	tgg	cac	acc	gtc	gcc	aaa	gag	aca	tgc	agt	gag	480
89	Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu	
90	145				150					155					160		
92	aag	agt	acc	aac	ttg	cat	gac	tac	ggc	atg	ttg	ctg	ccc	tgc	gga	att	528
93	Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile	
94				165				170					175				
96	gac	aag	ttc	cga	ggg	gta	gag	ttt	gtg	tgt	tgc	cca	ctg	gct	gaa	gaa	576
97	Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu	
98			180					185					190				
100	agt	gac	aat	gtg	gat	tct	gct	gat	gcg	gag	gag	gat	gac	tcg	gat	gtc	624
101	Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	
102			195					200					205				
104	tgg	tgg	ggc	gga	gca	gac	aca	gac	tat	gca	gat	ggg	agt	gaa	gac	aaa	672
105	Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys	
106		210					215					220					
108	gta	gta	gaa	gta	gca	gag	gag	gaa	gaa	gtg	gct	gag	gtg	gaa	gaa	gaa	720
109	Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	
110	225				230					235					240		
112	gaa	gcc	gat	gat	gac	gag	gac	gat	gag	gat	ggt	gat	gag	gta	gag	gaa	768
113	Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	
114				245				250					255				
116	gag	gct	gag	gaa	ccc	tac	gaa	gaa	gcc	aca	gag	aga	acc	acc	agc	att	816
117	Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	
118			260					265					270				
120	gcc	acc	acc	acc	acc	acc	acc	aca	gag	tct	gtg	gaa	gag	gtg	gtt	cga	864
121	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	
122			275					280					285				
124	gag	gtg	tgc	tct	gaa	caa	gcc	gag	acg	ggg	ccg	tgc	cga	gca	atg	atc	912
125	Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile	
126		290					295					300					
128	tcc	cgc	tgg	tac	ttt	gat	gtg	act	gaa	ggg	aag	tgt	gcc	cca	ttc	ttt	960
129	Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe	
130	305				310						315				320		
132	tac	ggc	gga	tgt	ggc	ggc	aac	cgg	aac	aac	ttt	gac	aca	gaa	gag	tac	1008
133	Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr	
134				325				330					335				
136	tgc	atg	gcc	gtg	tgt	ggc	agc	gcc	atg	tcc	caa	agt	tta	ctc	aag	act	1056

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137	Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr	
138				340					345					350			
140	acc	cag	gaa	cct	ctt	gcc	cga	gat	cct	gtt	aaa	ctt	cct	aca	aca	gca	1104
141	Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala	
142			355					360					365				
144	gcc	agt	acc	cct	gat	gcc	gtt	gac	aag	tat	ctc	gag	aca	cct	ggg	gat	1152
145	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	
146		370						375					380				
148	gag	aat	gaa	cat	gcc	cat	ttc	cag	aaa	gcc	aaa	gag	agg	ctt	gag	gcc	1200
149	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	
150	385					390					395					400	
152	aag	cac	cga	gag	aga	atg	tcc	cag	gtc	atg	aga	gaa	tgg	gaa	gag	gca	1248
153	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	
154				405					410					415			
156	gaa	cgt	caa	gca	aag	aac	ttg	cct	aaa	gct	gat	aag	aag	gca	gtt	atc	1296
157	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	
158			420						425					430			
160	cag	cat	ttc	cag	gag	aaa	gtg	gaa	tct	ttg	gaa	cag	gaa	gca	gcc	aac	1344
161	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	
162			435					440					445				
164	gag	aga	cag	cag	ctg	gtg	gag	aca	cac	atg	gcc	aga	gtg	gaa	gcc	atg	1392
165	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	
166		450					455					460					
168	ctc	aat	gac	cgc	cgc	cgc	ctg	gcc	ctg	gag	aac	tac	atc	acc	gct	ctg	1440
169	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	
170	465					470					475					480	
172	cag	gct	gtt	cct	cct	cgg	cct	cgt	cac	gtg	ttc	aat	atg	cta	aag	aag	1488
173	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	
174				485					490					495			
176	tat	gtc	cgc	gca	gaa	cag	aag	gac	aga	cag	cac	acc	cta	aag	cat	ttc	1536
177	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	
178			500					505					510				
180	gag	cat	gtg	cgc	atg	gtg	gat	ccc	aag	aaa	gcc	gct	cag	atc	cgg	tcc	1584
181	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	
182			515				520					525					
184	cag	gtt	atg	aca	cac	ctc	cgt	gtg	att	tat	gag	cgc	atg	aat	cag	tct	1632
185	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu	Arg	Met	Asn	Gln	Ser	
186		530					535					540					
188	ctc	tcc	ctg	ctc	tac	aac	gtg	cct	gca	gtg	gcc	gag	gag	att	cag	gat	1680
189	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala	Glu	Glu	Ile	Gln	Asp	
190	545					550					555					560	
192	gaa	gtt	gat	gag	ctg	ctt	cag	aaa	gag	caa	aac	tat	tca	gat	gac	gtc	1728
193	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn	Tyr	Ser	Asp	Asp	Val	
194				565					570					575			
196	ttg	gcc	aac	atg	att	agt	gaa	cca	agg	atc	agt	tac	gga	aac	gat	gct	1776
197	Leu	Ala	Asn	Met	Ile	Ser	Glu	Pro	Arg	Ile	Ser	Tyr	Gly	Asn	Asp	Ala	
198			580				585						590				
200	ctc	atg	cca	tct	ttg	acc	gaa	acg	aaa	acc	acc	gtg	gag	ctc	ctt	ccc	1824
201	Leu	Met	Pro	Ser	Leu	Thr	Glu	Thr	Lys	Thr	Thr	Val	Glu	Leu	Leu	Pro	

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202          595          600          605
204 gtg aat gga gag ttc agc ctg gac gat ctc cag ccg tgg cat tct ttt      1872
205 Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
206          610          615          620
208 ggg gct gac tct gtg cca gcc aac aca gaa aac gaa gtt gag cct gtt      1920
209 Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
210 625          630          635          640
212 gat gcc cgc cct gct gcc gac cga gga ctg acc act cga cca ggt tct      1968
213 Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
214          645          650          655
216 ggg ttg aca aat atc aag acg gag gag atc tct gaa gtg aag atg gat      2016
217 Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
218          660          665          670
220 gca gaa ttc cga cat gac tca gga tat gaa gtt cat cat caa aaa ttg      2064
221 Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
222          675          680          685
224 gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att gga      2112
225 Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
226          690          695          700
228 ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg atc gtc atc acc ttg      2160
229 Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
230 705          710          715          720
232 gtg atg ctg aag aag aaa cag tac aca tcc att cat cat ggt gtg gtg      2208
233 Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
234          725          730          735
236 gag gtt gac gcc gct gtc acc cca gag gag cgc cac ctg tcc aag atg      2256
237 Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
238          740          745          750
240 cag cag aac ggc tac gaa aat cca acc tac aag ttc ttt gag cag atg      2304
241 Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
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244 cag aac tag      2313
245 Gln Asn
246          770
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250 <211> LENGTH: 770
251 <212> TYPE: PRT
252 <213> ORGANISM: Homo sapiens
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262          20          25          30
265 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
266          35          40          45
269 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
270          50          55          60
273 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
274 65          70          75          80

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282					100					105					110	
285	Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu
286					115					120					125	
289	Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
290					130					135					140	
293	Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
294	145									150					155	
297	Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
298					165					170					175	
301	Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
302					180					185					190	
305	Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
306					195					200					205	
309	Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
310					210					215					220	
313	Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
314	225									230					235	
317	Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
318					245					250					255	
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322					260					265					270	
325	Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg
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329	Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile
330					290					295					300	
333	Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe
334	305									310					315	
337	Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Asn	Phe	Asp	Thr	Glu	Glu	Tyr
338					325					330					335	
341	Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr
342					340					345					350	
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346					355					360					365	
349	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp
350					370					375					380	
353	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala
354	385									390					395	
357	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala
358					405					410					415	
361	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile
362					420					425					430	
365	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn
366					435					440					445	
369	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met
370					450					455					460	
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